SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc.
Glucksmann, Maria
Meyers, Rachel

<120> 80090, 52874,52880,63497, AND 33425
METHODS AND COMPOSITIONS OF HUMAN PROTEINS AND USES THEREOF

<130> 38155-20044.00

<140> US 10/080,960
<141> 2001-10-19

<150> US 60/242,040
<151> 2000-10-20

<150> US 60/242,038
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ttttttttt ctttttggc cttggatacc gttgagaatc ta atg aaa gtc acg 174
Met Lys Val Thr
1

ggc cct ccc cag gga gtt aca gac tcc atg caa tgc ttc aat gat cag 222
Gly Pro Pro Gln Gly Val Thr Asp Ser Met Gln Cys Phe Asn Asp Gln
5 10 15 20

tgg cct tta tct aac acc agg agc agc gag cac ata aaa gag gtc atg 270
Trp Pro Leu Ser Asn Thr Arg Ser Ser Glu His Ile Lys Glu Val Met
25 30 35

gtt gag ctg ggg aag ttt gaa agg aag gag ttt aaa agt tcc agt ttg 318

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Val Glu Leu Gly Lys Phe Glu Arg Lys Glu Phe Lys Ser Ser Ser Leu
            40                  45                  50

caa gat gga cat aca aaa atg gag gaa gca cct acg cat ctt aat tca      366
Gln Asp Gly His Thr Lys Met Glu Glu Ala Pro Thr His Leu Asn Ser
        55                  60                  65

ttt ctt aag aaa gaa gga ttg acc ttc aac agg aaa aga aaa tgg gaa      414
Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys Arg Lys Trp Glu
    70                  75                  80

ttg gac agc tac ccc att atg ctc tgg tgg tcc ccg ctg acg ggg gag      462
Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro Leu Thr Gly Glu
85                  90                  95                  100

act ggg agg tta ggc caa tgt gga gca gat gct tgt ttc ttc acc atc      510
Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys Phe Phe Thr Ile
                105                 110                 115

aac cgg acc tac ctc cat cat cac atg acc aaa gca ttc ctc ttc tat      558
Asn Arg Thr Tyr Leu His His His Met Thr Lys Ala Phe Leu Phe Tyr
            120                 125                 130

ggt act gac ttt aac ata gat agc tta cct ctg cct cgg aaa gcc cat      606
Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro Arg Lys Ala His
        135                 140                 145

cat gac tgg gct gtt ttt cat gaa gag tcc ccg aaa aac aat tat aag      654
His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys Asn Asn Tyr Lys
    150                 155                 160

ctc ttt cat aaa cca gtg att acc ttg ttc aac tac act gcc acg ttc      702
Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr Thr Ala Thr Phe
165                 170                 175                 180

agc agg cat tcc cac ttg cca cta act acc caa tac ttg gag agc att      750
Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr Leu Glu Ser Ile
                185                 190                 195

gaa gtc ctg aag tca ctc cga tac cta gtt cct ttg cag tcc aaa aac      798
Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu Gln Ser Lys Asn
            200                 205                 210

aag ctt aga aaa aga ctt gct ccg ctg gtg tat gta cag tca gac tgt      846
Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val Gln Ser Asp Cys
        215                 220                 225

gac cca cca tca gac agg gac agc tat gtt cgc gag ctg atg act tac      894
Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu Leu Met Thr Tyr
    230                 235                 240

atc gag gtc gat tcc tat ggt gaa tgt tta cga aac aaa gac ctc cct      942
Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn Lys Asp Leu Pro
245                 250                 255                 260

cag cag ctg aaa aat cca gcc tct atg gat gcc gat ggc ttt tat agg      990
Gln Gln Leu Lys Asn Pro Ala Ser Met Asp Ala Asp Gly Phe Tyr Arg
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                265                 270                 275

atc att gca cag tat aag ttt atc cta gct ttt gag aat gca gtt tgt      1038
Ile Ile Ala Gln Tyr Lys Phe Ile Leu Ala Phe Glu Asn Ala Val Cys
            280                 285                 290

gat gac tac atc act gag aag ttc tgg agg cca ctg aaa ctg ggg gta      1086
Asp Asp Tyr Ile Thr Glu Lys Phe Trp Arg Pro Leu Lys Leu Gly Val
        295                 300                 305

gtc cct gta tat tac gga tcc ccc agc atc aca gac tgg ctt cca agt      1134
Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp Trp Leu Pro Ser
    310                 315                 320

aac aaa agt gct att ctt gta tca gaa ttt tct cac ccc agg gaa ctg      1182
Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His Pro Arg Glu Leu
325                 330                 335                 340

gca agt tac atc aga cga ctg gat tct gat gac aga ttg tat gag gcc      1230
Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg Leu Tyr Glu Ala
                345                 350                 355

tat gta gaa tgg aag ctg aag ggt gag atc tct aac cag cga ctt ctg      1278
Tyr Val Glu Trp Lys Leu Lys Gly Glu Ile Ser Asn Gln Arg Leu Leu
            360                 365                 370

aca gct ctc agg gaa cgg aaa tgg gga gtg caa gac gtc aac cag gac      1326
Thr Ala Leu Arg Glu Arg Lys Trp Gly Val Gln Asp Val Asn Gln Asp
        375                 380                 385

aat tac atc gat gca ttt gag tgt atg gtg tgc acc aag gtg tgg gct      1374
Asn Tyr Ile Asp Ala Phe Glu Cys Met Val Cys Thr Lys Val Trp Ala
    390                 395                 400

aat atc agg ctt cag gaa aag ggc tta cca ccc aaa aga tgg gag gca      1422
Asn Ile Arg Leu Gln Glu Lys Gly Leu Pro Pro Lys Arg Trp Glu Ala
405                 410                 415                 420

gaa gat acc cac ctg agt tgc cca gag ccc aca gtg ttt gct ttc tca      1470
Glu Asp Thr His Leu Ser Cys Pro Glu Pro Thr Val Phe Ala Phe Ser
                425                 430                 435

cca ctc cgg act cca cct ttg agc tct ttg cga gag atg tgg att tcc      1518
Pro Leu Arg Thr Pro Pro Leu Ser Ser Leu Arg Glu Met Trp Ile Ser
            440                 445                 450

agc ttt gaa caa tcc aag aaa gaa gcc cag gca cta agg tgg ctg gtt      1566
Ser Phe Glu Gln Ser Lys Lys Glu Ala Gln Ala Leu Arg Trp Leu Val
        455                 460                 465

gat agg aat caa aac ttt tca tct caa gag ttt tgg ggc cta gta ttc      1614
Asp Arg Asn Gln Asn Phe Ser Ser Gln Glu Phe Trp Gly Leu Val Phe
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Lys Asp  *
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aaaaaa

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Lys Glu Val Met Val Glu Leu Gly Lys Phe Glu Arg Lys Glu Phe Lys
        35                  40                  45
Ser Ser Ser Leu Gln Asp Gly His Thr Lys Met Glu Glu Ala Pro Thr
    50                  55                  60
His Leu Asn Ser Phe Leu Lys Lys Glu Gly Leu Thr Phe Asn Arg Lys
65                  70                  75                  80
Arg Lys Trp Glu Leu Asp Ser Tyr Pro Ile Met Leu Trp Trp Ser Pro
                85                  90                  95
Leu Thr Gly Glu Thr Gly Arg Leu Gly Gln Cys Gly Ala Asp Ala Cys
            100                 105                 110
Phe Phe Thr Ile Asn Arg Thr Tyr Leu His His His Met Thr Lys Ala
        115                 120                 125
Phe Leu Phe Tyr Gly Thr Asp Phe Asn Ile Asp Ser Leu Pro Leu Pro
    130                 135                 140
Arg Lys Ala His His Asp Trp Ala Val Phe His Glu Glu Ser Pro Lys
145                 150                 155                 160
Asn Asn Tyr Lys Leu Phe His Lys Pro Val Ile Thr Leu Phe Asn Tyr
                165                 170                 175
Thr Ala Thr Phe Ser Arg His Ser His Leu Pro Leu Thr Thr Gln Tyr
            180                 185                 190
Leu Glu Ser Ile Glu Val Leu Lys Ser Leu Arg Tyr Leu Val Pro Leu
        195                 200                 205
Gln Ser Lys Asn Lys Leu Arg Lys Arg Leu Ala Pro Leu Val Tyr Val
    210                 215                 220
Gln Ser Asp Cys Asp Pro Pro Ser Asp Arg Asp Ser Tyr Val Arg Glu
225                 230                 235                 240
Leu Met Thr Tyr Ile Glu Val Asp Ser Tyr Gly Glu Cys Leu Arg Asn
                245                 250                 255
Lys Asp Leu Pro Gln Gln Leu Lys Asn Pro Ala Ser Met Asp Ala Asp
            260                 265                 270
Gly Phe Tyr Arg Ile Ile Ala Gln Tyr Lys Phe Ile Leu Ala Phe Glu
        275                 280                 285
Asn Ala Val Cys Asp Asp Tyr Ile Thr Glu Lys Phe Trp Arg Pro Leu
    290                 295                 300
Lys Leu Gly Val Val Pro Val Tyr Tyr Gly Ser Pro Ser Ile Thr Asp
305                 310                 315                 320
Trp Leu Pro Ser Asn Lys Ser Ala Ile Leu Val Ser Glu Phe Ser His
                325                 330                 335
Pro Arg Glu Leu Ala Ser Tyr Ile Arg Arg Leu Asp Ser Asp Asp Arg
            340                 345                 350
Leu Tyr Glu Ala Tyr Val Glu Trp Lys Leu Lys Gly Glu Ile Ser Asn
        355                 360                 365
Gln Arg Leu Leu Thr Ala Leu Arg Glu Arg Lys Trp Gly Val Gln Asp
    370                 375                 380
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Val Asn Gln Asp Asn Tyr Ile Asp Ala Phe Glu Cys Met Val Cys Thr
385                 390                 395                 400
Lys Val Trp Ala Asn Ile Arg Leu Gln Glu Lys Gly Leu Pro Pro Lys
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Arg Trp Glu Ala Glu Asp Thr His Leu Ser Cys Pro Glu Pro Thr Val
            420                 425                 430
Phe Ala Phe Ser Pro Leu Arg Thr Pro Pro Leu Ser Ser Leu Arg Glu
        435                 440                 445
Met Trp Ile Ser Ser Phe Glu Gln Ser Lys Lys Glu Ala Gln Ala Leu
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Arg Trp Leu Val Asp Arg Asn Gln Asn Phe Ser Ser Gln Glu Phe Trp
465                 470                 475                 480
Gly Leu Val Phe Lys Asp
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aagtttgaaa ggaaggagtt taaaagttcc agtttgcaag atggacatac aaaaatggag     180
gaagcaccta cgcatcttaa ttcatttctt aagaaagaag gattgacctt caacaggaaa     240
agaaaatggg aattggacag ctaccccatt atgctctggt ggtccccgct gacgggggag     300
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aacaattata agctctttca taaaccagtg attaccttgt tcaactacac tgccacgttc     540
agcaggcatt cccacttgcc actaactacc caatacttgg agagcattga agtcctgaag     600
tcactccgat acctagttcc tttgcagtcc aaaaacaagc ttagaaaaag acttgctccg     660
ctggtgtatg tacagtcaga ctgtgaccca ccatcagaca gggacagcta tgttcgcgag     720
ctgatgactt acatcgaggt cgattcctat ggtgaatgtt tacgaaacaa agacctccct     780
cagcagctga aaaatccagc ctctatggat gccgatggct tttataggat cattgcacag     840
tataagttta tcctagcttt tgagaatgca gtttgtgatg actacatcac tgagaagttc     900
tggaggccac tgaaactggg ggtagtccct gtatattacg gatcccccag catcacagac     960
tggcttccaa gtaacaaaag tgctattctt gtatcagaat tttctcaccc cagggaactg    1020
gcaagttaca tcagacgact ggattctgat gacagattgt atgaggccta tgtagaatgg    1080
aagctgaagg gtgagatctc taaccagcga cttctgacag ctctcaggga acggaaatgg    1140
ggagtgcaag acgtcaacca ggacaattac atcgatgcat ttgagtgtat ggtgtgcacc    1200
aaggtgtggg ctaatatcag gcttcaggaa aagggcttac cacccaaaag atgggaggca    1260
gaagataccc acctgagttg cccagagccc acagtgtttg ctttctcacc actccggact    1320
ccacctttga gctctttgcg agagatgtgg atttccagct ttgaacaatc caagaaagaa    1380
gcccaggcac taaggtggct ggttgatagg aatcaaaact tttcatctca agagttttgg    1440
ggcctagtat tcaaggactg a                                              1461
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Leu His Phe Ala Gly Gly Tyr Leu Pro Ser Asp Ser Gln Asp Trp Arg
        10                  15                  20

acc atc atc ccg gct ctc ttg gtg gct gtc tgc ctg gtg ggc ttc gtg       148
Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys Leu Val Gly Phe Val
    25                  30                  35

gga aac ctg tgt gtg att ggc atc ctc ctc cac aat gct tgg aaa gga       196
Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His Asn Ala Trp Lys Gly
40                  45                  50                  55

aag cca tcc atg atc cac tcc ctg att ctg aat ctc agc ctg gct gat       244
Lys Pro Ser Met Ile His Ser Leu Ile Leu Asn Leu Ser Leu Ala Asp
                60                  65                  70

ctc tcc ctc ctg ctg ttt tct gca cct atc cga gct acg gcg tac tcc       292
Leu Ser Leu Leu Leu Phe Ser Ala Pro Ile Arg Ala Thr Ala Tyr Ser
            75                  80                  85

aaa agt gtt tgg gat cta ggc tgg ttt gtc tgc aag tcc tct gac tgg       340
Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys Lys Ser Ser Asp Trp
        90                  95                  100

ttt atc cac aca tgc atg gca gcc aag agc ctg aca atc gtt gtg gtg       388
Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu Thr Ile Val Val Val
    105                 110                 115

gcc aaa gta tgc ttc atg tat gca agt gac cca gcc aag caa gtg agt       436
Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro Ala Lys Gln Val Ser
120                 125                 130                 135

atc cac aac tac acc atc tgg tca gtg ctg gtg gcc atc tgg act gtg       484
Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val Ala Ile Trp Thr Val
                140                 145                 150

gct agc ctg tta ccc ctg ccg gaa tgg ttc ttt agc acc atc agg cat       532
Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe Ser Thr Ile Arg His
            155                 160                 165

cat gaa ggt gtg gaa atg tgc ctc gtg gat gta cca gct gtg gct gaa       580
His Glu Gly Val Glu Met Cys Leu Val Asp Val Pro Ala Val Ala Glu
        170                 175                 180

gag ttt atg tcg atg ttt ggt aag ctc tac cca ctc ctg gca ttt ggc       628
Glu Phe Met Ser Met Phe Gly Lys Leu Tyr Pro Leu Leu Ala Phe Gly
    185                 190                 195

ctt cca tta ttt ttt gcc agc ttt tat ttc tgg aga gct tat gac caa       676
Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp Arg Ala Tyr Asp Gln
200                 205                 210                 215

tgt aaa aaa cga gga act aag act caa aat ctt aga aac cag ata cgc       724
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Cys Lys Lys Arg Gly Thr Lys Thr Gln Asn Leu Arg Asn Gln Ile Arg
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tca aag caa gtc aca gtg atg ctg ctg agc att gcc atc atc tct gct      772
Ser Lys Gln Val Thr Val Met Leu Leu Ser Ile Ala Ile Ile Ser Ala
            235                 240                 245

ctc ttg tgg ctc ccc gaa tgg gta gct tgg ctg tgg gta tgg cat ctg      820
Leu Leu Trp Leu Pro Glu Trp Val Ala Trp Leu Trp Val Trp His Leu
        250                 255                 260

aag gct gca ggc ccg gcc cca cca caa ggt ttc ata gcc ctg tct caa      868
Lys Ala Ala Gly Pro Ala Pro Pro Gln Gly Phe Ile Ala Leu Ser Gln
    265                 270                 275

gtc ttg atg ttt tcc atc tct tca gca aat cct ctc att ttt ctt gtg      916
Val Leu Met Phe Ser Ile Ser Ser Ala Asn Pro Leu Ile Phe Leu Val
280                 285                 290                 295

atg tcg gaa gag ttc agg gaa ggc ttg aaa ggt gta tgg aaa tgg atg      964
Met Ser Glu Glu Phe Arg Glu Gly Leu Lys Gly Val Trp Lys Trp Met
                300                 305                 310

ata acc aaa aaa cct cca act gtc tca gag tct cag gaa aca cca gct     1012
Ile Thr Lys Lys Pro Pro Thr Val Ser Glu Ser Gln Glu Thr Pro Ala
            315                 320                 325

ggc aac tca gag ggt ctt cct gac aag gtc cca tct cca gaa tcc cca     1060
Gly Asn Ser Glu Gly Leu Pro Asp Lys Val Pro Ser Pro Glu Ser Pro
        330                 335                 340

gca tcc ata cca gaa aaa gag aaa ccc agc tct ccc tcc tct ggc aaa     1108
Ala Ser Ile Pro Glu Lys Glu Lys Pro Ser Ser Pro Ser Ser Gly Lys
    345                 350                 355

ggg aaa act gag aag gca gag att ccc atc ctt cct gac gta gag cag     1156
Gly Lys Thr Glu Lys Ala Glu Ile Pro Ile Leu Pro Asp Val Glu Gln
360                 365                 370                 375

ttt tgg cat gag agg gac aca gtc cct tct gta caa ttg aag agc acc     1204
Phe Trp His Glu Arg Asp Thr Val Pro Ser Val Gln Leu Lys Ser Thr
                380                 385                 390

aac cct aca gat tgt ggt agc tca ggt aac tca gcg tgg tac cgc aaa     1252
Asn Pro Thr Asp Cys Gly Ser Ser Gly Asn Ser Ala Trp Tyr Arg Lys
            395                 400                 405

act gaa aaa tca gca tgt tgc cct aag acg gaa atc cat tca aca ttc     1300
Thr Glu Lys Ser Ala Cys Cys Pro Lys Thr Glu Ile His Ser Thr Phe
        410                 415                 420

tac ttc cag ata ctg ctt cta gca att cac aga aac aga aac cac atc     1348
Tyr Phe Gln Ile Leu Leu Leu Ala Ile His Arg Asn Arg Asn His Ile
    425                 430                 435

tca cgt ttc tca act aaa caa ctg ctt tta gga ctg cag cac aag ttc     1396
Ser Arg Phe Ser Thr Lys Gln Leu Leu Leu Gly Leu Gln His Lys Phe
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            20                  25                  30
Val Cys Leu Val Gly Phe Val Gly Asn Leu Cys Val Ile Gly Ile Leu
        35                  40                  45
Leu His Asn Ala Trp Lys Gly Lys Pro Ser Met Ile His Ser Leu Ile
    50                  55                  60
Leu Asn Leu Ser Leu Ala Asp Leu Ser Leu Leu Leu Phe Ser Ala Pro
65                  70                  75                  80
Ile Arg Ala Thr Ala Tyr Ser Lys Ser Val Trp Asp Leu Gly Trp Phe
                85                  90                  95
Val Cys Lys Ser Ser Asp Trp Phe Ile His Thr Cys Met Ala Ala Lys
            100                 105                 110
Ser Leu Thr Ile Val Val Val Ala Lys Val Cys Phe Met Tyr Ala Ser
        115                 120                 125
Asp Pro Ala Lys Gln Val Ser Ile His Asn Tyr Thr Ile Trp Ser Val
    130                 135                 140
Leu Val Ala Ile Trp Thr Val Ala Ser Leu Leu Pro Leu Pro Glu Trp
145                 150                 155                 160
Phe Phe Ser Thr Ile Arg His His Glu Gly Val Glu Met Cys Leu Val
                165                 170                 175
Asp Val Pro Ala Val Ala Glu Glu Phe Met Ser Met Phe Gly Lys Leu
            180                 185                 190
Tyr Pro Leu Leu Ala Phe Gly Leu Pro Leu Phe Phe Ala Ser Phe Tyr
        195                 200                 205
Phe Trp Arg Ala Tyr Asp Gln Cys Lys Lys Arg Gly Thr Lys Thr Gln
    210                 215                 220
Asn Leu Arg Asn Gln Ile Arg Ser Lys Gln Val Thr Val Met Leu Leu
225                 230                 235                 240
Ser Ile Ala Ile Ile Ser Ala Leu Leu Trp Leu Pro Glu Trp Val Ala
                245                 250                 255
Trp Leu Trp Val Trp His Leu Lys Ala Ala Gly Pro Ala Pro Pro Gln
            260                 265                 270
Gly Phe Ile Ala Leu Ser Gln Val Leu Met Phe Ser Ile Ser Ser Ala
        275                 280                 285
Asn Pro Leu Ile Phe Leu Val Met Ser Glu Glu Phe Arg Glu Gly Leu
    290                 295                 300
Lys Gly Val Trp Lys Trp Met Ile Thr Lys Lys Pro Pro Thr Val Ser
305                 310                 315                 320
Glu Ser Gln Glu Thr Pro Ala Gly Asn Ser Glu Gly Leu Pro Asp Lys
                325                 330                 335
Val Pro Ser Pro Glu Ser Pro Ala Ser Ile Pro Glu Lys Glu Lys Pro
            340                 345                 350
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Ser Ser Pro Ser Ser Gly Lys Gly Lys Thr Glu Lys Ala Glu Ile Pro
        355                 360                 365
Ile Leu Pro Asp Val Glu Gln Phe Trp His Glu Arg Asp Thr Val Pro
    370                 375                 380
Ser Val Gln Leu Lys Ser Thr Asn Pro Thr Asp Cys Gly Ser Ser Gly
385                 390                 395                 400
Asn Ser Ala Trp Tyr Arg Lys Thr Glu Lys Ser Ala Cys Cys Pro Lys
                405                 410                 415
Thr Glu Ile His Ser Thr Phe Tyr Phe Gln Ile Leu Leu Leu Ala Ile
            420                 425                 430
His Arg Asn Arg Asn His Ile Ser Arg Phe Ser Thr Lys Gln Leu Leu
        435                 440                 445
Leu Gly Leu Gln His Lys Phe Arg Phe Ser Val Phe Pro
    450                 455                 460
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<213> Homo sapiens

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aacctgtgtg tgattggcat cctcctccac aatgcttgga aaggaaagcc atccatgatc 180
cactccctga ttctgaatct cagcctggct gatctctccc tcctgctgtt ttctgcacct 240
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atctggtcag tgctggtggc catctggact gtggctagcc tgttaccccct gccggaatgg 480
ttctttagca ccatcaggca tcatgaaggt gtggaaatgt gcctcgtgga tgtaccagct 540
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ccattatttt ttgccagctt ttatttctgg agagcttatg accaatgtaa aaaacgagga 660
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aactcagcgt ggtaccgcaa aactgaaaaa tcagcatgtt gccctaagac ggaaatccat 1260
tcaacattct acttccagat actgcttcta gcaattcaca gaaacagaaa ccacatctca 1320
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<221> CDS
<222> (210)...(1301)

<400> 7
tactcactat agggctcgag cggccgcccg ggcaggtcta gaattcagcg gccgctgaat 60

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tctaggctgc tctgggcctt gctagccggc tctgcacctc ccagaagccg tgggcacgcc   120
gctcagctgc tccatcgcct cactttccca ggctcgcgcc cgaagcagag ccatgagaac   180
cccagggtgc ctggcgagcc gctagcgcc atg ggc ccc ggc gag gcg ctg ctg      233
                               Met Gly Pro Gly Glu Ala Leu Leu
                                 1               5

gcg ggt ctt ctg gtg atg gta ctg gcc gtg gcg ctg cta tcc aac gca      281
Ala Gly Leu Leu Val Met Val Leu Ala Val Ala Leu Leu Ser Asn Ala
     10                  15                  20

ctg gtg ctg ctt tgt tgc gcc tac agc gct gag ctc cgt act cga gcc      329
Leu Val Leu Leu Cys Cys Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala
 25                  30                  35                  40

tca ggc gtc ctc ctg gtg aat ctg tcg ctg ggc cac ctg ctg ctg gcg      377
Ser Gly Val Leu Leu Val Asn Leu Ser Leu Gly His Leu Leu Leu Ala
                 45                  50                  55

gcg ctg gac atg ccc ttc acg ctg ctc ggt gtg atg cgc ggg cgg aca      425
Ala Leu Asp Met Pro Phe Thr Leu Leu Gly Val Met Arg Gly Arg Thr
             60                  65                  70

ccg tcg gcg ccc ggc gca tgc caa gtc att ggc ttc ctg gac acc ttc      473
Pro Ser Ala Pro Gly Ala Cys Gln Val Ile Gly Phe Leu Asp Thr Phe
         75                  80                  85

ctg gcg tcc aac gcg gcg ctg agc gtg gcg gcg ctg agc gca gac cag      521
Leu Ala Ser Asn Ala Ala Leu Ser Val Ala Ala Leu Ser Ala Asp Gln
     90                  95                  100

tgg ctg gca gtg ggc ttc cca ctg cgc tac gcc gga cgc ctg cga ccg      569
Trp Leu Ala Val Gly Phe Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro
105                 110                 115                 120

cgc tat gcc ggc ctg ctg ctg ggc tgt gcc tgg gga cag tcg ctg gcc      617
Arg Tyr Ala Gly Leu Leu Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala
                125                 130                 135

ttc tca ggc gct gca ctt ggc tgc tcg tgg ctt ggc tac agc agc gcc      665
Phe Ser Gly Ala Ala Leu Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala
            140                 145                 150

ttc gcg tcc tgt tcg ctg cgc ctg ccg ccc gag cct gag cgt ccg cgc      713
Phe Ala Ser Cys Ser Leu Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg
        155                 160                 165

ttc gca gcc ttc acc gcc acg ctc cat gcc gtg ggc ttc gtg ctg ccg      761
Phe Ala Ala Phe Thr Ala Thr Leu His Ala Val Gly Phe Val Leu Pro
    170                 175                 180

ctg gcg gtg ctc tgc ctc acc tcg ctc cag gtg cac cgg gtg gca cgc      809
Leu Ala Val Leu Cys Leu Thr Ser Leu Gln Val His Arg Val Ala Arg
185                 190                 195                 200

agc cac tgc cag cgc atg gac act gtc acc atg aag gcg ctc gcg ctg      857
Ser His Cys Gln Arg Met Asp Thr Val Thr Met Lys Ala Leu Ala Leu
                205                 210                 215
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ctc gcc gac ctg cac ccc agt gtg cgg cag cgc tgc ctc atc cag cag      905
Leu Ala Asp Leu His Pro Ser Val Arg Gln Arg Cys Leu Ile Gln Gln
            220                 225                 230

aag cgg cgc cgc cac cgc gcc acc agg aag att ggc att gct att gcg      953
Lys Arg Arg Arg His Arg Ala Thr Arg Lys Ile Gly Ile Ala Ile Ala
        235                 240                 245

acc ttc ctc atc tgc ttt gcc ccg tat gtc atg acc agg ctg gcg gag     1001
Thr Phe Leu Ile Cys Phe Ala Pro Tyr Val Met Thr Arg Leu Ala Glu
    250                 255                 260

ctc gtg ccc ttc gtc acc gtg aac gcc cag tgg ggc atc ctc agc aag     1049
Leu Val Pro Phe Val Thr Val Asn Ala Gln Trp Gly Ile Leu Ser Lys
265                 270                 275                 280

tgc ctg acc tac agc aag gcg gtg gcc gac ccg ttc acg tac tct ctg     1097
Cys Leu Thr Tyr Ser Lys Ala Val Ala Asp Pro Phe Thr Tyr Ser Leu
                285                 290                 295

ctc cgc cgg ccg ttc cgc caa gtc ctg gcc ggc atg gtg cac cgg ctg     1145
Leu Arg Arg Pro Phe Arg Gln Val Leu Ala Gly Met Val His Arg Leu
            300                 305                 310

ctg aag aga acc ccg cgc cca gca tcc acc cat gac agc tct ctg gat     1193
Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asp Ser Ser Leu Asp
        315                 320                 325

gtg gcc ggc atg gtg cac cag ctg ctg aag aga acc ccg cgc cca gcg     1241
Val Ala Gly Met Val His Gln Leu Leu Lys Arg Thr Pro Arg Pro Ala
    330                 335                 340

tcc acc cac aac ggc tct gtg gac aca gag aat gat tcc tgc ctg cag     1289
Ser Thr His Asn Gly Ser Val Asp Thr Glu Asn Asp Ser Cys Leu Gln
345                 350                 355                 360

cag aca cac tga gggcctggca gggctcatcg cccccacctt ctaagaagcc         1341
Gln Thr His  *

ctgtggaaag a                                                        1352

<210> 8
<211> 363
<212> PRT
<213> Homo sapiens

<400> 8
Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu
 1               5                  10                  15
Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr
            20                  25                  30
Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
        35                  40                  45
Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
    50                  55                  60
```

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Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
65                  70                  75                  80
Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
                85                  90                  95
Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
            100                 105                 110
Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
        115                 120                 125
Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
    130                 135                 140
Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
145                 150                 155                 160
Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
                165                 170                 175
His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
            180                 185                 190
Leu Gln Val His Arg Val Ala Arg Ser His Cys Gln Arg Met Asp Thr
        195                 200                 205
Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val
    210                 215                 220
Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr
225                 230                 235                 240
Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
                245                 250                 255
Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn
            260                 265                 270
Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
        275                 280                 285
Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
    290                 295                 300
Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala
305                 310                 315                 320
Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
                325                 330                 335
Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp
            340                 345                 350
Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His
        355                 360
```

<210> 9
<211> 1092
<212> DNA
<213> Homo sapiens

<400> 9

```
atgggccccg gcgaggcgct gctggcgggt cttctggtga tggtactggc cgtggcgctg      60
ctatccaacg cactggtgct gctttgttgc gcctacagcg ctgagctccg tactcgagcc     120
tcaggcgtcc tcctggtgaa tctgtcgctg ggccacctgc tgctggcggc gctggacatg     180
cccttcacgc tgctcggtgt gatgcgcggg cggacaccgt cggcgcccgg cgcatgccaa     240
gtcattggct tcctggacac cttcctggcg tccaacgcgg cgctgagcgt ggcggcgctg     300
agcgcagacc agtggctggc agtgggcttc ccactgcgct acgccggacg cctgcgaccg     360
cgctatgccg gcctgctgct gggctgtgcc tggggacagt cgctggcctt ctcaggcgct     420
gcacttggct gctcgtggct tggctacagc agcgccttcg cgtcctgttc gctgcgcctg     480
ccgcccgagc ctgagcgtcc gcgcttcgca gccttcaccg ccacgctcca tgccgtgggc     540
ttcgtgctgc cgctggcggt gctctgcctc acctcgctcc aggtgcaccg ggtggcacgc     600
agccactgcc agcgcatgga cactgtcacc atgaaggcgc tcgcgctgct cgccgacctg     660
caccccagtg tgcggcagcg ctgcctcatc cagcagaagc ggcgccgcca ccgcgccacc     720
```

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aggaagattg gcattgctat tgcgaccttc ctcatctgct ttgccccgta tgtcatgacc     780
aggctggcgg agctcgtgcc cttcgtcacc gtgaacgccc agtggggcat cctcagcaag     840
tgcctgacct acagcaaggc ggtggccgac ccgttcacgt actctctgct ccgccggccg     900
ttccgccaag tcctggccgg catggtgcac cggctgctga agagaacccc gcgcccagca     960
tccacccatg acagctctct ggatgtggcc ggcatggtgc accagctgct gaagagaacc    1020
ccgcgcccag cgtccaccca caacggctct gtggacacag agaatgattc ctgcctgcag    1080
cagacacact ga                                                       1092

<210> 10
<211> 1178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (152)...(1057)

<400> 10
ctgtgacttt aagtatttct aagggcagag caatgggagg tggagaatgc tgggttgcag      60
gtgacactat aaacgtagat catgcctcct atttccatgc aggacctccc agccctgaag     120
acaaacatca gtgacagaca tcagtggcag a atg gcc tcc cgg tat gtg gca         172
                                    Met Ala Ser Arg Tyr Val Ala
                                     1               5

gtg gga atg atc tta tca cag acc gtg gtg gga gtc ctg ggg agc ttc       220
Val Gly Met Ile Leu Ser Gln Thr Val Val Gly Val Leu Gly Ser Phe
         10                  15                  20

tct gtt ctt ctc cat tat ctc tcc ttt tac tgc act ggg tgc agg tta       268
Ser Val Leu Leu His Tyr Leu Ser Phe Tyr Cys Thr Gly Cys Arg Leu
     25                  30                  35

agg tcc aca gat ttg att gtt aag cac ctg att gta gcc aac ttc tta       316
Arg Ser Thr Asp Leu Ile Val Lys His Leu Ile Val Ala Asn Phe Leu
 40                  45                  50                  55

gct ctc cgc tgt aaa gga gtc ccc cag aca atg gca gct ttt ggg gtt       364
Ala Leu Arg Cys Lys Gly Val Pro Gln Thr Met Ala Ala Phe Gly Val
                 60                  65                  70

aga tat ttt ctc aat gct ctt ggg tgc aaa ctt gtt ttc tat ctc cat       412
Arg Tyr Phe Leu Asn Ala Leu Gly Cys Lys Leu Val Phe Tyr Leu His
             75                  80                  85

aga gtg ggc agg gga gtg tcc att ggc acc acc tgc ctc ttg agt gtc       460
Arg Val Gly Arg Gly Val Ser Ile Gly Thr Thr Cys Leu Leu Ser Val
         90                  95                  100

ttc cag gtg atc acg gtc agc tcc agg aaa tcc agg tgg gca aaa ctt       508
Phe Gln Val Ile Thr Val Ser Ser Arg Lys Ser Arg Trp Ala Lys Leu
    105                 110                 115

aaa gag aaa gcc ccc aag cat gtt ggc ttt tct gtt ctc ctg tgc tgg       556
Lys Glu Lys Ala Pro Lys His Val Gly Phe Ser Val Leu Leu Cys Trp
120                 125                 130                 135

atc gtg tgc atg ttg gta aac atc atc ttt ccc atg tat gtg gct ggc       604
```

```
Ile Val Cys Met Leu Val Asn Ile Ile Phe Pro Met Tyr Val Ala Gly
                140                 145                 150

aaa tgg aac tac aca aac atc aca gtg aac gag gat ttg gga tac tgt      652
Lys Trp Asn Tyr Thr Asn Ile Thr Val Asn Glu Asp Leu Gly Tyr Cys
            155                 160                 165

tct ggg gga ggc aac aac aaa atc gca cag aca ctg cgt gca atg ttg      700
Ser Gly Gly Gly Asn Asn Lys Ile Ala Gln Thr Leu Arg Ala Met Leu
        170                 175                 180

tta tca ttc cct gat gtg ttg tgt ctg ggg ctc atg ttc tgg gtc agc      748
Leu Ser Phe Pro Asp Val Leu Cys Leu Gly Leu Met Phe Trp Val Ser
    185                 190                 195

agc tcc atg gtt tgc ata ctg cac agg cac aag cag cgg gtc cag cac      796
Ser Ser Met Val Cys Ile Leu His Arg His Lys Gln Arg Val Gln His
200                 205                 210                 215

att gat agg agc gat ctc tcc ccc aga gcc tcc cca gag aac aga gct      844
Ile Asp Arg Ser Asp Leu Ser Pro Arg Ala Ser Pro Glu Asn Arg Ala
                220                 225                 230

acg cag agc atc ctc atc ctg gtg agc acc ttt gtg tct tct tac act      892
Thr Gln Ser Ile Leu Ile Leu Val Ser Thr Phe Val Ser Ser Tyr Thr
            235                 240                 245

ctc tcc tgc ctt ttc caa gtt tgt atg gct ctt ttg gat aat ccc aat      940
Leu Ser Cys Leu Phe Gln Val Cys Met Ala Leu Leu Asp Asn Pro Asn
        250                 255                 260

agt tta ctg gtg aac act tca gcc tta atg agt gta tgt ttc cca act      988
Ser Leu Leu Val Asn Thr Ser Ala Leu Met Ser Val Cys Phe Pro Thr
    265                 270                 275

ctc agc ccc ttt gtt ctc atg agc tgt gac ccc agt gta tac agg ttt     1036
Leu Ser Pro Phe Val Leu Met Ser Cys Asp Pro Ser Val Tyr Arg Phe
280                 285                 290                 295

tgt ttt gcc tgg aaa aga tga caagatctcc taacctcatc ataaacatgt      1087
Cys Phe Ala Trp Lys Arg  *
                300

acattgtata tatttgctca tggttcaatt gatgacttac tcttctgtgc cgcaacctgc  1147
ccgggcggcc gctcgagccc tatagtgagt a                                 1178

<210> 11
<211> 301
<212> PRT
<213> Homo sapiens

<400> 11
Met Ala Ser Arg Tyr Val Ala Val Gly Met Ile Leu Ser Gln Thr Val
 1               5                  10                  15
Val Gly Val Leu Gly Ser Phe Ser Val Leu Leu His Tyr Leu Ser Phe
            20                  25                  30
Tyr Cys Thr Gly Cys Arg Leu Arg Ser Thr Asp Leu Ile Val Lys His
```

```
        35                  40                  45
Leu Ile Val Ala Asn Phe Leu Ala Leu Arg Cys Lys Gly Val Pro Gln
    50                  55                  60
Thr Met Ala Ala Phe Gly Val Arg Tyr Phe Leu Asn Ala Leu Gly Cys
65                  70                  75                  80
Lys Leu Val Phe Tyr Leu His Arg Val Gly Arg Gly Val Ser Ile Gly
                85                  90                  95
Thr Thr Cys Leu Leu Ser Val Phe Gln Val Ile Thr Val Ser Ser Arg
            100                 105                 110
Lys Ser Arg Trp Ala Lys Leu Lys Glu Lys Ala Pro Lys His Val Gly
        115                 120                 125
Phe Ser Val Leu Leu Cys Trp Ile Val Cys Met Leu Val Asn Ile Ile
    130                 135                 140
Phe Pro Met Tyr Val Ala Gly Lys Trp Asn Tyr Thr Asn Ile Thr Val
145                 150                 155                 160
Asn Glu Asp Leu Gly Tyr Cys Ser Gly Gly Gly Asn Asn Lys Ile Ala
                165                 170                 175
Gln Thr Leu Arg Ala Met Leu Leu Ser Phe Pro Asp Val Leu Cys Leu
            180                 185                 190
Gly Leu Met Phe Trp Val Ser Ser Ser Met Val Cys Ile Leu His Arg
        195                 200                 205
His Lys Gln Arg Val Gln His Ile Asp Arg Ser Asp Leu Ser Pro Arg
    210                 215                 220
Ala Ser Pro Glu Asn Arg Ala Thr Gln Ser Ile Leu Ile Leu Val Ser
225                 230                 235                 240
Thr Phe Val Ser Ser Tyr Thr Leu Ser Cys Leu Phe Gln Val Cys Met
                245                 250                 255
Ala Leu Leu Asp Asn Pro Asn Ser Leu Leu Val Asn Thr Ser Ala Leu
            260                 265                 270
Met Ser Val Cys Phe Pro Thr Leu Ser Pro Phe Val Leu Met Ser Cys
        275                 280                 285
Asp Pro Ser Val Tyr Arg Phe Cys Phe Ala Trp Lys Arg
    290                 295                 300
```

<210> 12
<211> 906
<212> DNA
<213> Homo sapiens

<400> 12

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atggcctccc ggtatgtggc agtgggaatg atcttatcac agaccgtggt gggagtcctg      60
gggagcttct ctgttcttct ccattatctc tccttttact gcactgggtg caggttaagg     120
tccacagatt tgattgttaa gcacctgatt gtagccaact tcttagctct ccgctgtaaa     180
ggagtccccc agacaatggc agcttttggg gttagatatt ttctcaatgc tcttgggtgc     240
aaacttgttt tctatctcca tagagtgggc aggggagtgt ccattggcac cacctgcctc     300
ttgagtgtct tccaggtgat cacggtcagc tccaggaaat ccaggtgggc aaaacttaaa     360
gagaaagccc ccaagcatgt tggcttttct gttctcctgt gctggatcgt gtgcatgttg     420
gtaaacatca tctttcccat gtatgtggct ggcaaatgga actacacaaa catcacagtg     480
aacgaggatt tgggatactg ttctgggggа ggcaacaaca aaatcgcaca gacactgcgt     540
gcaatgttgt tatcattccc tgatgtgttg tgtctggggc tcatgttctg ggtcagcagc     600
tccatggttt gcatactgca caggcacaag cagcgggtcc agcacattga taggagcgat     660
ctctccccca gagcctcccc agagaacaga gctacgcaga gcatcctcat cctggtgagc     720
acctttgtgt cttcttacac tctctcctgc cttttccaag tttgtatggc tcttttggat     780
aatcccaata gtttactggt gaacacttca gccttaatga gtgtatgttt cccaactctc     840
agccccttg ttctcatgag ctgtgacccc agtgtataca ggttttgttt tgcctggaaa     900
agatga                                                               906
```

<210> 13
<211> 3492
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73)...(2064)

<400> 13
tgccaggcga gacaggaact tctttcccct tctctgtgtc aggatcgcag aaagtatgtc 60
ccttctctca cc atg agc tgg ctc tcc agt tcc cag gga gtg gta cta aca 111
Met Ser Trp Leu Ser Ser Ser Gln Gly Val Val Leu Thr
1 5 10

gcc tac cac ccc agc ggc aag gac cag gcc gtc ggg aac agc cat gca 159
Ala Tyr His Pro Ser Gly Lys Asp Gln Ala Val Gly Asn Ser His Ala
15 20 25

aag gca ggg gag gaa gcc acc tcg agt cgc aga tat ggc cag tac act 207
Lys Ala Gly Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
30 35 40 45

atg aac cag gaa agc acc acc atc aaa gtt atg gag aag cct cca ttt 255
Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe
50 55 60

gat cga tca att tcc cag gat tct ttg gat gaa cta tct atg gaa gac 303
Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp
65 70 75

tat tgg ata gaa cta gaa aac atc aag aaa tct agt gaa aac agc caa 351
Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln
80 85 90

gaa gat caa gag gtg gtt gtt gtc aaa gag cct gat gag gga gaa ttg 399
Glu Asp Gln Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu
95 100 105

gaa gaa gag tgg ctt aaa gag gcc ggt tta tcc aat ctc ttc gga gag 447
Glu Glu Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu
110 115 120 125

tct gct gga gat cca cag gaa agc att gtg ttt tta tca aca ttg acg 495
Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr
130 135 140

cgg acc cag gca gca gca gtt cag aag cga gta gag acg gtc tcc cag 543
Arg Thr Gln Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln
145 150 155

acc ttg aga aaa aaa aac aaa cag tac cag att cct gac gtc aga gac 591
Thr Leu Arg Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp
160 165 170

ata ttt gct caa cag aga gaa tca aaa gaa aca gct cca ggt ggc act 639
Ile Phe Ala Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr

```
    175                 180                 185

gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa gga aga gat      687
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp
190                 195                 200                 205

gac gag gca tct aac ctt gtt ggt gaa gag aag ctg atc cca cct gag      735
Asp Glu Ala Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu
                210                 215                 220

gag acg cct gcc cct gaa aca gac atc aac ctg gag gta tca ttt gcc      783
Glu Thr Pro Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala
            225                 230                 235

gag caa gca ctc aat cag aaa gag agc tcc aag gag aaa atc cag aag      831
Glu Gln Ala Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys
        240                 245                 250

agc aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca aaa gac      879
Ser Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp
    255                 260                 265

aaa acg ggt acc aca agg att ggt gac ctc gca ccc cag gac atg aag      927
Lys Thr Gly Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys
270                 275                 280                 285

aaa gtt tgc cat tta gcc cta att gag ctg act gcc ctc tat gat gta      975
Lys Val Cys His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val
                290                 295                 300

ttg ggt att gag ctg aaa caa caa aaa gct gtg aaa atc aaa aca aaa     1023
Leu Gly Ile Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys
            305                 310                 315

gat tct ggt ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa gat     1071
Asp Ser Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp
        320                 325                 330

cag agg aaa gta cca gga atg cga ata ccc ttg atc ttt caa aaa ctg     1119
Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu
    335                 340                 345

att tct cga att gaa gag aga ggt ttg gaa aca gaa ggc ctc tta cgg     1167
Ile Ser Arg Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg
350                 355                 360                 365

atc cct gga gct gcc att aga atc aag aat ctt tgc caa gaa cta gaa     1215
Ile Pro Gly Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu
                370                 375                 380

gca aag ttt tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat     1263
Ala Lys Phe Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His
            385                 390                 395

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg ccc cag cca     1311
Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro
        400                 405                 410
```

```
ctg ctc agt gtg gag tat ctc aaa gcc ttt cag gct gtc cag aat ctt      1359
Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu
    415                 420                 425

cca acc aag aag cag caa cta cag gct ttg aac ctt ctt gtc atc ctc      1407
Pro Thr Lys Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Val Ile Leu
430                 435                 440                 445

cta cct gat gca aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc      1455
Leu Pro Asp Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu
                450                 455                 460

caa aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc atg aat      1503
Gln Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn
            465                 470                 475

gta gca atg gtc atg gcc ccg aat ctc ttt atg tgt cat gca ttg gga      1551
Val Ala Met Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly
        480                 485                 490

ttg aag tcc agt gaa cag cga gaa ttt gta atg gca gct ggg aca gca      1599
Leu Lys Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala
    495                 500                 505

aat acc atg cac tta ttg att aag tac caa aaa ctt ctg tgg aca att      1647
Asn Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile
510                 515                 520                 525

ccc aag ttt att gta aac caa gtg agg aag caa aac acg gaa aat cat      1695
Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His
                530                 535                 540

aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag aaa atg gct tat      1743
Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr
            545                 550                 555

gac cga gaa aaa tat gaa aag caa gat aag agt aca aat gat gct gac      1791
Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp
        560                 565                 570

gtt cct cag gga gtg att cga gtg caa gct ccc cat ctt tcg aaa gtt      1839
Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val
    575                 580                 585

tcc atg gca ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt      1887
Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu
590                 595                 600                 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act ctc aag aaa      1935
Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys
                610                 615                 620

gga gaa gtt ttt ttg tat gaa att gga gga aat att ggg gaa cgc tgc      1983
Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys
            625                 630                 635
```

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ctt gat gat gac act tac atg aag gat tta tat cag ctt aac cca aat     2031
Leu Asp Asp Asp Thr Tyr Met Lys Asp Leu Tyr Gln Leu Asn Pro Asn
       640                 645                 650

gct gag tgg gtt ata aag tca aag cca ttg tag aagacttaac aagctgcaga   2084
Ala Glu Trp Val Ile Lys Ser Lys Pro Leu  *
    655                 660

taaccatgtg gacttctgtc ataattcttg ctgagtcaag agtgtaaata aaagaaatgg   2144
caggactcat attattcagt tgtacccaag tatttaaaaa tgactctctt aagccttaaa   2204
aagtcataga tttgtgctgc tgccagaatt atattaatta ttattaatgt tattattaga   2264
aaaaaaattt ctggagtgag agtaaagagg cttaattagt ttgtgggcag ttttcatatg   2324
ctctgtgaaa tgtgtccaga tgtgacatag ttttttttt ttaatatgtg gaaatgtctt   2384
ctcttcccat tcttttctcc taaaatcata tatactgtaa tatatgctct ctcacctcta   2444
ttacctcctc acatctaccc tttcccagtt aggtttgctt tttgaccaaa aagataacaa   2504
ataccaggta tggcaagttg tgaagacagc acattaaaac atacctaatt tcacagtatt   2564
cctgtcacga cagaatgtta gtattcatct ctttgaatca tttgctcaaa taataacatt   2624
ccacctttc ctgctgtatc acaggaagtg atttgcattt tttttcagtt catctgactt   2684
atgttcacag aaccgtatca gcgaccaaga aaataggact gtcagaagct gccagttatt   2744
actgaaccat taaatactta tatactaaga ataaataaaa tatacccatg tgaaataata   2804
attggattat ggataacaag agagtgaaag ccaaagcact ttctgtctac tgtactcttc   2864
taaatggaat tttaaaagtc atagctggct ttacgtgttg tcattattag cattataaat   2924
atgcatgata gtataatcca gtaatggttg aagaatgtat tttacttaaa gagggatttt   2984
ttttttaag tcctgaataa gtctactgga agaattattc ttctgggtga aaaagctttt   3044
gtttgtgttc ttattttaaa taatcggagt caatttatta aaatgttctt gaaagtacta   3104
ttcccaggga ttttaatgca caaaccatat tgtgacaaga gatgagcctc tgtactgtaa   3164
ataagaaatg aagtagagaa atgttaaata ttttatgagt ttagaatata gtaaataaaa   3224
ggtgatgtaa atgaatgctg cacaaacggt gttcatgata cttttagtag tactttagga   3284
aaaactacac attctcagaa gctcttgatg tctctaatga agggggggaa tgctgttaat   3344
gagaacagtc ataaattttt agcatataat tacaagaaca gcctgtggat atgatcactt   3404
aaatgatttt gtggtgattc gtgccattgc ttttttattt aaaagaaaat tttgtaatta   3464
aatgcctttt tctaaaaaaa aaaaaaaa                                      3492
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<210> 14
<211> 663
<212> PRT
<213> Homo sapiens

<400> 14

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Met Ser Trp Leu Ser Ser Ser Gln Gly Val Val Leu Thr Ala Tyr His
 1               5                  10                  15
Pro Ser Gly Lys Asp Gln Ala Val Gly Asn Ser His Ala Lys Ala Gly
            20                  25                  30
Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln
        35                  40                  45
Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser
    50                  55                  60
Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile
65                  70                  75                  80
Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln
                85                  90                  95
Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu
            100                 105                 110
Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly
        115                 120                 125
Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr Arg Thr Gln
    130                 135                 140
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Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg
145 150 155 160
Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
165 170 175
Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln
180 185 190
Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala
195 200 205
Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro
210 215 220
Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala
225 230 235 240
Leu Asn Gln Lys Glu Ser Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly
245 250 255
Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly
260 265 270
Thr Thr Arg Ile Gly Asp Leu Ala Pro Gln Asp Met Lys Lys Val Cys
275 280 285
His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile
290 295 300
Glu Leu Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser Gly
305 310 315 320
Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys
325 330 335
Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
340 345 350
Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
355 360 365
Ala Ala Ile Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
370 375 380
Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His Asp Ala Ala
385 390 395 400
Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser
405 410 415
Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys
420 425 430
Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp
435 440 445
Ala Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val
450 455 460
Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met
465 470 475 480
Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys Ser
485 490 495
Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
500 505 510
His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
515 520 525
Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
530 535 540
Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu
545 550 555 560
Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln
565 570 575
Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
580 585 590
Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe

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        595                 600                 605
Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val
    610                 615                 620
Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp
625                 630                 635                 640
Asp Thr Tyr Met Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp
                645                 650                 655
Val Ile Lys Ser Lys Pro Leu
            660
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<210> 15
<211> 1992
<212> DNA
<213> Homo sapiens

<400> 15

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atgagctggc tctccagttc ccagggagtg gtactaacag cctaccaccc cagcggcaag      60
gaccaggccg tcgggaacag ccatgcaaag gcaggggagg aagccacctc gagtcgcaga     120
tatggccagt acactatgaa ccaggaaagc accaccatca aagttatgga gaagcctcca     180
tttgatcgat caatttccca ggattctttg gatgaactat ctatggaaga ctattggata     240
gaactagaaa acatcaagaa atctagtgaa aacagccaag aagatcaaga ggtggttgtt     300
gtcaaagagc ctgatgaggg agaattggaa gaagagtggc ttaaagaggc cggtttatcc     360
aatctcttcg gagagtctgc tggagatcca caggaaagca ttgtgttttt atcaacattg     420
acgcggaccc aggcagcagc agttcagaag cgagtagaga cggtctccca gaccttgaga     480
aaaaaaaaca aacagtacca gattcctgac gtcagagaca tatttgctca acagagagaa     540
tcaaaagaaa cagctccagg tggcactgaa tcgcagtcac ttagaacaaa tgaaaacaaa     600
taccaaggaa gagatgacga ggcatctaac cttgttggtg aagagaagct gatcccacct     660
gaggagacgc ctgcccctga aacagacatc aacctggagg tatcatttgc cgagcaagca     720
ctcaatcaga aagagagctc caaggagaaa atccagaaga gcaaaggcga tgatgccaca     780
ttacctagtt tcagattgcc aaaagacaaa acgggtacca caaggattgg tgacctcgca     840
ccccaggaca tgaagaaagt ttgccattta gccctaattg agctgactgc cctctatgat     900
gtattgggta ttgagctgaa acaacaaaaa gctgtgaaaa tcaaaacaaa agattctggt     960
ctttttgcg ttccattgac agcgctatta gaacaagatc agaggaaagt accaggaatg    1020
cgaataccct tgatctttca aaaactgatt tctcgaattg aagagagagg tttggaaaca    1080
gaaggcctct tacggatccc tggagctgcc attagaatca agaatctttg ccaagaacta    1140
gaagcaaagt tttatgaagg gacttttaat tgggaaagtg tcaaacagca tgatgccgcc    1200
agcctgctga agctcttcat tcgggagttg ccccagccac tgctcagtgt ggagtatctc    1260
aaagcctttc aggctgtcca gaatcttcca accaagaagc agcaactaca ggctttgaac    1320
cttcttgtca tcctcctacc tgatgcaaac agggacacac tgaaggccct tcttgaattt    1380
ctccaaagag taatagataa taaagaaaaa aataaaatga cagtcatgaa tgtagcaatg    1440
gtcatggccc cgaatctctt tatgtgtcat gcattgggat tgaagtccag tgaacagcga    1500
gaatttgtaa tggcagctgg gacagcaaat accatgcact tattgattaa gtaccaaaaa    1560
cttctgtgga caattcccaa gtttattgta aaccaagtga ggaagcaaaa cacggaaaat    1620
cataaaaagg ataaaagagc catgaagaaa ttgctgaaga aaatggctta tgaccgagaa    1680
aaatatgaaa agcaagataa gagtacaaat gatgctgacg ttcctcaggg agtgattcga    1740
gtgcaagctc cccatctttc gaaagtttcc atggcaatac agctaactga agaactaaaa    1800
gccagtgatg tacttgccag gtttctcagc caagaaagtg gggttgccca gactctcaag    1860
aaaggagaag ttttttgta tgaaattgga ggaaatattg gggaacgctg ccttgatgat     1920
gacacttaca tgaaggattt atatcagctt aacccaaatg ctgagtgggt tataaagtca    1980
aagccattgt ag                                                       1992
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<210> 16
<211> 502
<212> PRT
<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 16

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Leu Ser Asp Ala Phe Leu Arg Leu Leu Trp Arg Glu Lys Leu Leu Gly
 1               5                  10                  15
Leu Leu Ile Thr Val Pro Pro Leu Leu Leu Ala Ile Ala Ala Trp Ile
            20                  25                  30
Gly Leu Glu Glu Ile Lys Glu Trp Lys Lys Ser Pro Leu Tyr Leu Ser
        35                  40                  45
Asn Asp His Glu Leu Asp Val Pro Ile Leu Leu Ile Leu Ser Gln Ala
    50                  55                  60
Pro Gln Gly Ser Arg Phe Pro Thr Leu Glu Glu Asn Arg Ile Leu Leu
65                  70                  75                  80
Trp Thr Trp Pro Phe Asn Asp Arg Gly Ala Pro Val Pro Pro Ser Arg
                85                  90                  95
Cys Ser Leu Ser Tyr Asp Asn Thr Ala Arg Cys Arg Leu Thr Ala Asn
            100                 105                 110
Arg Ser Glu Leu Glu Ser Ala Asp Ala Val Leu Phe Asn Ala Gly His
        115                 120                 125
His Arg Asp Leu Ser Lys Gly Pro Pro Met Asp Leu Pro Pro Glu Phe
    130                 135                 140
Thr Gln Val Arg Ala Arg Ala Glu Asp Ala Asp Ala Val Leu Leu Ala
145                 150                 155                 160
Tyr Glu Asp Asn Ala Ala Ala Ala Glu Ala Leu Ala Thr Asp Phe Pro
                165                 170                 175
Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser Pro Ser
            180                 185                 190
Asn Ser Gly Arg Phe Ala Val Pro Gly Phe Lys Ile Asn Val Leu Asn
        195                 200                 205
Gly Leu Gln Ile Leu Leu Asp Gly Tyr Phe Asn Trp Thr Leu Ser Tyr
    210                 215                 220
Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly Tyr Leu Glu Pro Leu
225                 230                 235                 240
Thr Ala Lys Ala Arg Lys Arg Gly Phe Lys Val Gln Ser Gln Val Val
                245                 250                 255
Glu Ala Pro Leu Asn Leu Ser Ala Lys Ala Lys Leu Ala Ala Trp Val
            260                 265                 270
Val Ser Asn Cys Asn Thr Arg Ser Lys Arg Glu Arg Phe Tyr Lys Gln
        275                 280                 285
Leu Lys Lys His Leu Gln Val Asp Val Tyr Gly Arg Val Ala Asn Pro
    290                 295                 300
Leu Pro Leu Lys Ser Gly Cys Ser Lys Gly Val Glu Leu Ile Glu Thr
305                 310                 315                 320
Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Glu
                325                 330                 335
Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu Gln Ala Gly Thr
            340                 345                 350
Ile Pro Val Val Leu Gly Pro Ser Arg Ala Val Tyr Glu Asp Phe Val
        355                 360                 365
Pro Pro Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser Ala Lys Glu
    370                 375                 380
Leu Ala Asp Tyr Leu Leu Tyr Leu Asp Lys Asn Pro Thr Ala Tyr Leu
385                 390                 395                 400
Asp Met Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala Tyr
                405                 410                 415
Phe Tyr Gln Asp Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys Thr
            420                 425                 430
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Ile Leu Glu Asn Asp Thr Ile Tyr His Lys Tyr Ser Glu Tyr Phe Glu
435 440 445
Trp Arg Glu Asp Leu Arg Val Arg Leu Phe Ser Trp Asp Ala Leu Arg
450 455 460
Val Leu Glu Tyr Asp Glu Gly Phe Cys Arg Val Cys Arg Leu Leu Gln
465 470 475 480
Lys Ala Pro Asp Leu Leu Glu Leu Ser Arg Tyr Lys Thr Ile Pro Asn
485 490 495
Leu Ala Lys Trp Phe Gln
500

<210> 17
<211> 178
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 17
Pro Val Glu Leu Val Trp Trp Ser Arg Asp Met Ser Trp Asn Tyr Asp
1 5 10 15
Val Gln Arg Gln Cys Gly Ile His Thr Cys Arg Ile Thr Asn Lys Arg
20 25 30
Ser Arg Arg Pro Trp Ala Arg Gly Val Leu Phe Tyr Gly Ser Asn Ile
35 40 45
Lys Thr Gly Asp Phe Pro Leu Pro Arg Asn Glu His Gln Ile Trp Ala
50 55 60
Leu Leu His Glu Glu Ser Pro Arg Asn Thr Pro Phe Val Ser Asn Lys
65 70 75 80
Glu Phe Leu Arg His Phe His Phe Thr Ser Thr Phe Ser Arg Tyr Ser
85 90 95
Asn Leu Pro Leu Thr Thr Met Tyr Leu Pro Ser Gly Glu Ala Leu Thr
100 105 110
Ser Lys Asp Tyr Tyr Val Thr Phe Asp Gly Lys Ser Lys Tyr Gly Tyr
115 120 125
Arg Pro Ser Thr Ser Val Val Phe Leu Gln Ser Asp Cys Asp Thr Met
130 135 140
Ser Gly Arg Glu Asp Tyr Val Lys Glu Leu Met Lys His Leu Pro Ile
145 150 155 160
Asp Ser Tyr Gly Ser Cys Leu Arg Asn Arg Asp Leu Pro Glu Arg Gln
165 170 175
Lys Asp

<210> 18
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 18
Val Ala Trp Val Val Ser Asn Trp Asn Pro Asn Ser Ala Arg Val Arg
1 5 10 15
Tyr Tyr Gln Gln Leu Gln Lys His Leu Lys Val Asp Val Tyr Gly Arg

```
            20                  25                  30
Ser His Arg Gly Lys Pro Leu Pro Gln Gly Asn Met Met Glu Thr Leu
        35                  40                  45
Ser Arg Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Met His Pro Asp
    50                  55                  60
Tyr Ile Thr Glu Lys Leu Trp Arg Asn Ala Leu Glu Ala Gly Ala Val
65                  70                  75                  80
Pro Val Val Leu Gly Pro Ser Arg Val Asn Tyr Glu Arg Phe Ile Pro
                85                  90                  95
Pro Asp Ala Phe Ile His Val Asp Asp Phe Gln Ser Pro Lys Glu Leu
            100                 105                 110
Ala Lys Tyr Leu Lys Glu Leu Asp Lys Asn His Ala Ala Tyr Leu Lys
        115                 120                 125
Tyr Leu Arg Trp Lys Tyr Glu Asn Pro Leu Asn
    130                 135

<210> 19
<211> 296
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 19
Ile Leu Leu Trp Asn Glu Pro Ser Leu Val Asn Ala Pro Ala His Val
 1               5                  10                  15
Glu Cys Gly Cys Leu Val Thr Thr Ser Arg Ser His Asn Asp Lys Ala
            20                  25                  30
Phe Asp Ala Val Val Ile Ser Ala Asp His Pro Tyr Ser Phe Glu Gly
        35                  40                  45
Leu Gly Gly Val Lys Leu His Pro Asp Phe Tyr Ala Val Tyr Ala Ala
    50                  55                  60
Lys Lys Pro Leu Ser Ser Thr Gln Asn Pro Leu Thr Asn Phe Thr Leu
65                  70                  75                  80
Pro Pro Phe Asn Leu Thr Met Thr Tyr Arg Leu Asp Ser Gln Leu Ile
                85                  90                  95
Trp Thr Asp Tyr Tyr Phe Ser His Thr Asn Leu Ala Arg Arg Leu Lys
            100                 105                 110
Trp Phe Arg Ala Pro Ser Lys Ser Phe Ala Asp Asp Met Pro Ala Thr
        115                 120                 125
Thr Val Leu Arg Leu Glu Ser Glu Ile Leu Lys Lys Ser Arg Leu Ala
    130                 135                 140
Val Tyr Leu Val Tyr Glu Val Asn Glu Lys Thr Leu Pro Glu Ser Leu
145                 150                 155                 160
Tyr Met Glu Glu Leu Arg Lys Tyr Ala Asp Leu Asp Ala His Asp Asn
                165                 170                 175
Cys Leu Gly Thr Asp Asp His Tyr His Phe Met Leu Ile Phe Glu Thr
            180                 185                 190
Ser Ala Cys Pro Asp Tyr Val Pro Pro Gln Met Ser Met Ala Met Asp
        195                 200                 205
Lys Leu Leu Val Pro Val Leu Ile Gly Gly Gly Asn Leu Thr Asn Leu
    210                 215                 220
Val Pro Ser His Ser Tyr Ile Ser Ser Gln Asp Phe Ala Thr Pro Gln
225                 230                 235                 240
Asp Leu Ile Ile His Leu Lys Asp Leu Ala Asn Asn Gln Leu Glu Tyr
                245                 250                 255
```

```
Arg Arg Tyr Phe Trp Trp His Ser Ile Tyr Arg Leu Arg Lys Thr Ser
            260                 265                 270
Gln Pro Tyr Cys Ala Leu Cys Ser Leu Ile Gln Gln Ser Pro Gly Gly
        275                 280                 285
His Glu Val Arg Gln Arg Ser Tyr
    290                 295
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<210> 20
<211> 81
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 20

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Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
 1               5                  10                  15
Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
            20                  25                  30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
        35                  40                  45
Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
    50                  55                  60
Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65                  70                  75                  80
Ser
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<210> 21
<211> 155
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 21

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Lys Val Val Ile Leu Leu Val Trp Val Leu Ala Leu Leu Leu Ser Leu
 1               5                  10                  15
Pro Pro Leu Leu Phe Ser Trp Val Lys Thr Val Glu Glu Gly Asn Gly
            20                  25                  30
Thr Leu Asn Val Asn Val Thr Val Cys Leu Ile Asp Phe Pro Glu Glu
        35                  40                  45
Ser Thr Ala Ser Val Ser Thr Trp Leu Arg Ser Tyr Val Leu Leu Ser
    50                  55                  60
Thr Leu Val Gly Phe Leu Leu Pro Leu Leu Val Ile Leu Val Cys Tyr
65                  70                  75                  80
Thr Arg Ile Leu Arg Thr Leu Arg Lys Ala Ala Lys Thr Leu Leu Val
                85                  90                  95
Val Val Val Val Phe Val Leu Cys Trp Leu Pro Tyr Phe Ile Val Leu
            100                 105                 110
Leu Leu Asp Thr Leu Cys Leu Ser Ile Ile Met Ser Ser Thr Cys Glu
        115                 120                 125
Leu Glu Arg Val Leu Pro Thr Ala Leu Leu Val Thr Leu Trp Leu Ala
    130                 135                 140
Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr
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145 150 155

<210> 22
<211> 65
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 22
Glu Trp Thr Glu Trp Leu Tyr Asp Val Tyr His Tyr Phe His Met Val
1 5 10 15
Ser Gly Val Leu Phe Tyr Leu Ser Ser Ala Ile Asn Pro Ile Leu Tyr
20 25 30
Asn Leu Met Ser His Arg Phe Arg Glu Ala Phe Lys Asn Val Leu Ser
35 40 45
Ser Leu Cys Lys Gln Trp His Ser Arg His Lys Pro Arg Pro Ser Phe
50 55 60
Ser
65

<210> 23
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 23
Tyr Phe Lys Ile Ile Leu Lys Met Cys Gln Arg Lys Arg Gln Met Gln
1 5 10 15
Thr Lys Arg Thr Ala Thr Lys Lys Arg Thr Thr Lys Val Thr Ile Met
20 25 30
Gly Leu Ala Ile Val Ile Ser Tyr Thr His Cys Trp Leu Pro Phe Trp
35 40 45
Ile Val Gln Trp Ser Ile Glu Ala Asn Leu Phe Glu Lys Ser Lys Tyr
50 55 60
Leu Leu Phe Cys Cys Thr His Phe Ala Phe Ala Leu Gln Tyr Ile Asn
65 70 75 80
Ser Ala Ala Asn Pro Phe Leu Tyr Val Phe Leu Ser Asp Ser Phe Gln
85 90 95
Lys Asn Ile Gln Lys Leu Leu Arg Thr Ala Lys Pro
100 105

<210> 24
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 24
Pro Ser Asp Ala Pro Glu Thr Tyr Ser Asp Thr Val Leu Ser Val Val
1 5 10 15

Leu Gly Phe Tyr Ala Leu Leu Leu Leu Ile Ala Phe Ala Ser Asn Ile
20 25 30
Leu Leu Ala Gly Val Ile Lys Lys Tyr Arg Trp Gly Met Lys Met Ala
35 40 45
Leu Leu Phe His Leu Cys Val Thr Gly Ala Leu Leu Ser Ile Thr Asn
50 55 60
Thr Leu His Leu Leu Ala Ser Gly Tyr His Leu Leu Lys Arg Gln Arg
65 70 75 80
Asn Ser Ser Thr Val Leu Gln Ser Phe Ala Ile Ile Ala Trp Val Asp
85 90 95
His Phe Ile Gly Phe Ala Leu Leu Ile Phe Val Met Tyr Leu Ala Ile
100 105 110
Phe Cys Phe Lys Phe Tyr Trp Asn Asn Lys Thr Arg Ser Ile Glu Trp
115 120 125
Gly Arg Ser Tyr Val Leu Tyr Ala Ile Ser Thr Trp Val Ile Ala Phe
130 135 140
Leu Ile Ala Gly Phe Thr Ala Phe Phe Gln Cys Asp Ser His Ile Asn
145 150 155 160
Ser Gln Asp Gln Cys Ile Gln Ile Val Cys Ala Val Ser Asn Ile Phe
165 170 175
Ser Ala Ile Phe Thr Glu Leu
180

<210> 25
<211> 259
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 25
Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
1 5 10 15
Thr Pro Thr Asn Ile Phe Ile Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30
Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45
Ser Glu Asp Trp Pro Phe Gly Ser Ala Leu Cys Lys Leu Val Thr Ala
50 55 60
Leu Asp Val Val Asn Met Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile
65 70 75 80
Ser Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg
85 90 95
Arg Arg Thr Ser Pro Arg Arg Ala Lys Val Val Ile Leu Leu Val Trp
100 105 110
Val Leu Ala Leu Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Val
115 120 125
Lys Thr Val Glu Glu Gly Asn Gly Thr Leu Asn Val Asn Val Thr Val
130 135 140
Cys Leu Ile Asp Phe Pro Glu Glu Ser Thr Ala Ser Val Ser Thr Trp
145 150 155 160
Leu Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Leu Leu Pro
165 170 175
Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg
180 185 190
Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe Val Leu Cys

195 200 205
Trp Leu Pro Tyr Phe Ile Val Leu Leu Leu Asp Thr Leu Cys Leu Ser
210 215 220
Ile Ile Met Ser Ser Thr Cys Glu Leu Glu Arg Val Leu Pro Thr Ala
225 230 235 240
Leu Leu Val Thr Leu Trp Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro
245 250 255

Ile Ile Tyr

<210> 26
<211> 182
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 26
Ala Leu Thr Phe Pro Ala Thr Ala Leu Ala Leu Ser Trp Leu Gly Phe
1 5 10 15
His Gln Leu Tyr Ala Ser Cys Thr Leu Cys Ser Arg Arg Pro Asp Glu
20 25 30
Arg Leu Arg Phe Ala Val Phe Thr Ser Ala Phe His Ala Leu Ser Phe
35 40 45
Leu Leu Ser Phe Ile Val Leu Cys Phe Thr Tyr Leu Lys Val Leu Lys
50 55 60
Val Ala Arg Phe His Cys Lys Arg Ile Asp Val Ile Thr Met Gln Thr
65 70 75 80
Leu Val Leu Leu Val Asp Ile His Pro Ser Val Arg Glu Arg Cys Leu
85 90 95
Glu Glu Gln Lys Arg Arg Arg Gln Arg Ala Thr Lys Lys Ile Ser Thr
100 105 110
Phe Ile Gly Thr Phe Leu Val Cys Phe Ala Pro Tyr Val Ile Thr Arg
115 120 125
Leu Val Glu Leu Phe Ser Thr Ala Pro Ile Asp Ser His Trp Gly Val
130 135 140
Leu Ser Lys Cys Leu Ala Tyr Ser Lys Ala Ala Ser Asp Pro Phe Val
145 150 155 160
Tyr Ser Leu Leu Arg His Gln Tyr Arg Arg Ser Cys Lys Glu Leu Leu
165 170 175
Asn Arg Ile Phe Asn Arg
180

<210> 27
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 27
Thr Leu Phe Ile Val Gly Phe Met Ile Pro Cys Leu Val Ile Ile Val
1 5 10 15
Cys Tyr Ala Cys Ile Phe Leu Thr Val His His Gln Lys Lys Lys Ile
20 25 30

Arg Asn His Asp Asn Phe Gln Ile Ala Ala Ala Lys Gly Ser Ser Ser
35 40 45
Ser Gly Gly Gly Ser Tyr Met Thr Thr Thr Cys Thr Arg Lys Ala Arg
50 55 60
Glu Asp Arg Lys Thr Thr Lys Met Leu Met Val Val Phe Leu Cys Phe
65 70 75 80
Ala Ile Cys Tyr Leu Pro Ile Ser Ile Leu Asn Val Leu Lys Arg Val
85 90 95
Phe Gly Met Phe Arg His Ser Glu Asp Asn Glu Ser Val Tyr Trp Trp
100 105 110
His Ile Phe Ser His Trp Leu Val Tyr Ala Asn Ser Cys Ile Asn Pro
115 120 125
Ile Ile Tyr Asn Phe Met Asn Gly Lys Tyr Arg Lys Ala Tyr Trp Lys
130 135 140
Ile Phe Ala Leu Leu Lys Phe Trp Gly Glu Pro Leu Ser
145 150 155

<210> 28
<211> 160
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 28
Ala Tyr Val Val Met Leu Val Val Ala Val Phe Phe Ile Pro Phe Ser
1 5 10 15
Val Met Leu Tyr Ser Tyr Met Cys Ile Leu Asn Thr Val Arg His Asn
20 25 30
Ala Val Arg Ile His Asn His Pro Asp Ser Leu Cys Leu Ser Gln Val
35 40 45
Ser Lys Leu Gly Leu Met Ser Leu Gln Arg Pro His Gln Met Ser Val
50 55 60
Asp Met Ser Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe
65 70 75 80
Val Gly Phe Ser Leu Cys Trp Leu Pro His Ser Val Tyr Ser Leu Leu
85 90 95
Ser Val Phe Ser Lys His Phe Tyr Tyr Gln His Asn Phe Tyr Glu Ile
100 105 110
Ser Thr Cys Val Leu Trp Leu Cys Tyr Leu Lys Ser Val Phe Asn Pro
115 120 125
Ile Ile Tyr Cys Trp Arg Ile Lys Lys Phe Arg Glu Ala Cys Leu Glu
130 135 140
Met Met Pro Lys Thr Phe Lys Ile Leu Pro Gln Val Pro Gly Arg Thr
145 150 155 160

<210> 29
<211> 93
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<400> 29
His Lys Ile Ile Lys Ala Ala Cys Leu Val Gln Gln Lys Arg Gln Glu

```
 1               5                  10                  15
Phe Leu Ala Ser Val Ala Arg Gly Val Ala Pro Ala Asp Ser Pro Glu
            20                  25                  30
Ala Pro Arg Arg Ser Phe Ala Gly Gly Thr Trp Asp Trp Glu Tyr Leu
        35                  40                  45
Gly Phe Ala Ser Pro Glu Glu Tyr Ala Glu Phe Gln Tyr Arg Arg Arg
    50                  55                  60
His Arg Gln Arg Arg Arg Gly Asp Val His Ser Leu Leu Ser Asn Pro
65                  70                  75                  80
Pro Asp Pro Asp Glu Pro Ser Glu Ser Thr Leu Asp Ile
                85                  90
```

<210> 30
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

```
<400> 30
Leu Leu Pro Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg
 1               5                  10                  15
Thr Leu Arg Lys Ala Ala Lys Thr Leu Leu Val Val Val Val Val Phe
            20                  25                  30
Val
```

<210> 31
<211> 260
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

```
<400> 31
Gly His Arg Ser Arg Pro Thr Asp Leu Pro Ile Gly Leu Leu Ser Leu
 1               5                  10                  15
Val His Leu Met Met Leu Leu Thr Met Gly Phe Ile Ala Thr Met Asp
            20                  25                  30
Met Phe Met Ser Trp Gly Arg Trp Asp Asp Thr Thr Cys Lys Ser Leu
        35                  40                  45
Ile Tyr Leu His Arg Leu Leu Arg Gly Leu Ser Leu Cys Thr Thr Cys
    50                  55                  60
Leu Leu Asn Val Phe Gln Ala Ile Thr Leu Ser Pro Arg Ser Ser Cys
65                  70                  75                  80
Leu Ala Lys Phe Lys His Lys Ser Pro His His Ile Ser Cys Ala Phe
                85                  90                  95
Leu Phe Leu Trp Val Leu Tyr Met Ser Phe Ser Ser His Leu Leu Leu
            100                 105                 110
Ser Ile Ile Ala Thr Pro Asn Leu Thr Ser Asn Asp Phe Met Tyr Val
        115                 120                 125
Thr Gln Ser Cys Ser Ile Leu Pro Met Ser Tyr Ser Met Gln Ser Met
    130                 135                 140
Phe Ser Thr Leu Leu Ala Ile Arg Asp Val Phe Leu Ile Gly Leu Met
145                 150                 155                 160
```

```
Val Leu Ser Ser Gly Tyr Met Val Ala Leu Leu Cys Arg His Arg Lys
                165                 170                 175
Gln Ala Gln His Leu His Ser Thr Ser Leu Ser Pro Lys Ala Ser Pro
            180                 185                 190
Glu Gln Arg Ala Thr Arg Thr Ile Leu Met Leu Met Ser Ser Phe Phe
        195                 200                 205
Val Leu Met Tyr Ile Phe Asp Ser Ile Val Phe Cys Ser Arg Thr Met
    210                 215                 220
Phe Lys Asp Gly Pro Thr Phe Tyr Cys Ile Gln Ile Ile Val Ser His
225                 230                 235                 240
Ser Tyr Ala Thr Val Ser Pro Phe Val Phe Ile Cys Thr Glu Lys His
                245                 250                 255
Ile Val Lys Phe
            260
```

<210> 32
<211> 170
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid

```
<400> 32
Pro Ile Ile Val Glu Lys Cys Val Glu Tyr Ile Glu Lys Leu Tyr Pro
 1               5                  10                  15
Leu Ala Glu Arg Gly Leu Gln Glu Glu Gly Ile Tyr Arg Val Ser Gly
            20                  25                  30
Ser Ala Ser Arg Val Lys Glu Leu Arg Glu Ala Phe Asp Lys Asp Gly
        35                  40                  45
Ala Pro Asp Ser Leu Glu Leu Ser Glu Lys Glu Trp Phe Asp Val His
    50                  55                  60
Val Val Ala Gly Leu Leu Lys Leu Tyr Leu Arg Glu Leu Pro Glu Pro
65                  70                  75                  80
Leu Ile Pro Tyr Asp Leu Tyr Glu Glu Phe Ile Arg Ala Ala Lys Glu
                85                  90                  95
Gln Ile Glu Asp Pro Asp Glu Arg Leu Arg Ala Leu Lys Glu Leu Leu
            100                 105                 110
Ser Ser Lys Leu Pro Arg Ala His Tyr Asn Thr Leu Arg Tyr Leu Leu
        115                 120                 125
Thr His Leu Asn Arg Val Ala Glu Ile Tyr Ile Glu Asn Ser Ala Val
    130                 135                 140
Asn Lys Met Asn Ala Arg Asn Leu Ala Ile Val Phe Gly Pro Thr Leu
145                 150                 155                 160
Leu Arg Pro Pro Asp Lys Glu Ser Asn Asp
                165                 170
```

<210> 33
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

```
<400> 33
Leu Lys Tyr Gln Lys Ile Leu Trp Lys Val Pro Ser Phe Leu Ile Thr
```

```
 1               5                  10                  15
Gln Val Arg Arg Met Asn Glu Ala Thr Met Leu Leu Lys Lys Gln Leu
            20                  25                  30
Pro Ser Val Arg Lys Leu Leu Arg Arg Lys Thr Leu Glu Arg Glu Thr
        35                  40                  45
Ala Ser Pro Lys Thr Ser Lys Val Leu Gln Lys Ser Pro Ser Ala Arg
    50                  55                  60
Arg Met Ser Asp Val Pro Glu Gly Val Ile Arg Val His Ala Pro Leu
65                  70                  75                  80
Leu Ser Lys Val Ser Met Ala Ile Gln Leu Asn Asn Gln Thr Lys Ala
                85                  90                  95
Lys Asp Ile Leu Ala Lys Phe
            100
```

<210> 34
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

```
<400> 34
Asn Met Glu Glu Tyr Glu Asp Val His Thr Val Ala Gly Leu Leu Lys
 1               5                  10                  15
Gln Tyr Phe Arg Glu Leu Pro Glu Pro Leu Leu Thr Tyr Glu Leu Tyr
            20                  25                  30
Glu Glu Phe Ile Glu Ala Ala Lys Ala Gln Val Ser Asp Glu Asp Glu
        35                  40                  45
Arg Met Glu Ala Leu Glu Met Leu Lys Glu Leu Ile Lys Leu Leu Pro
    50                  55                  60
Glu Ala Asn Arg Glu Thr Leu Arg Tyr Leu Leu Lys His Leu Ser Arg
65                  70                  75                  80
Val Ala Gln His Ser Glu Glu Asn Lys Met Asn Ala Gln Asn Leu Ala
                85                  90                  95
Val Val Phe Gly Pro Thr Leu
            100
```

<210> 35
<211> 90
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

```
<400> 35
Ala Cys Ser Leu Leu Lys Leu Phe Leu Arg Glu Leu Pro Glu Pro Leu
 1               5                  10                  15
Leu Thr Thr Asp Leu Val Ala Arg Phe Glu Glu Val Ala Ser His Pro
            20                  25                  30
Lys Val Thr Thr Gln Gln Ala Glu Leu Gln Gln Leu Leu Glu Gln Leu
        35                  40                  45
Pro Lys Cys Asn Arg Thr Leu Leu Ala Trp Val Leu Leu His Phe Asp
    50                  55                  60
Ala Val Ile Gln Gln Glu Arg His Asn Lys Leu Asn Ala Gln Ser Leu
65                  70                  75                  80
```

```
Ala Met Leu Leu Ser Pro Thr Leu Gln Met
                85                  90

<210> 36
<211> 79
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<221> VARIANT
<222> (1)...(79)
<223> Xaa = Any Amino Acid

<400> 36
Gly Ser Thr Ala Leu Ile Val Met Phe Tyr Trp Cys Gly Ser Thr Ala
 1               5                  10                  15
Asn Cys Pro Asp Glu Glu Asp Pro Lys Arg His Xaa Xaa Leu Ile Val
            20                  25                  30
Met Asn Gln Gly Ala Xaa Xaa Leu Ile Val Met Phe Thr Gly Ser Thr
        35                  40                  45
Ala Asn Cys Leu Ile Val Met Phe Tyr Trp Ser Thr Ala Cys Asp Glu
    50                  55                  60
Asn His Arg Phe Tyr Trp Cys Ser His Xaa Xaa Leu Ile Val Met
65                  70                  75

<210> 37
<211> 50
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus amino acid sequence

<221> VARIANT
<222> (1)...(50)
<223> Xaa = Any Amino Acid

<400> 37
Leu Ile Val Met Phe Trp Ala Cys Pro Gly Ala Cys Xaa Xaa Xaa Ser
 1               5                  10                  15
Ala Cys Lys Ser Thr Ala Leu Ile Met Arg Gly Ser Ala Cys Pro Asn
            20                  25                  30
Val Ser Thr Ala Cys Pro Xaa Xaa Asp Glu Asn Phe Ala Pro Xaa Xaa
        35                  40                  45
Ile Tyr
    50
```